FIGURE 1A

Organism	Di-potassium EDTA	ım EDTA	Di-ammonium EDTA	ium EDTA	Di-sodium EDTA	n EDTA	Tri- sodi	Tri- sodium EDTA	Tetra-sodium EDTA	ım EDTA
Œ	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC
S24 Staph. epidermidis	<0.5	8	<0.5	4	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
31 Staph. epidermidis	<0.5	8	<0.5	8	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
301 Staph. xylosus	<0.5	9	<0.5	4	<0.5	<0.5	<0.5	<0.5	<0.5	20
300 Staph.capitis	<0.5	10	<0.5	8	<0.5	<0.5	<0.5	<0.5	<0.5	10
J46 Staph.lentus	<0.5	10	<0.5	10	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
S24 Staph.capitis	<0.5	8	<0.5	10	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
R8 Staph.	<0.5	8	<0.5	10	<0.5	1	<0.5	1.5	<0.5	1
72 S.aureus	1	9	1	9	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
R57 S.aureus	1	8	1	10	<0.5	10	<0.5	<0.5	<0.5	8
R13 S.aureus	1	9	1	15	<0.5	10	<0.5	<0.5	<0.5	<0.5
R30 S.aureus	1	8	1	15	<0.5	10	<0.5	<0.5		1
8 S.aureus	1	8	1	10	<0.5	<0.5	<0.5	<0.5		
R64 MRSA	1	9	1	8	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5

FIGURE 1B

Organism	Di-potassium EDTA		Di-ammonium EDTA	ium EDTA	Di-sodium EDTA	n EDTA	Tri- sodi	Tri- sodium EDTA	Tetra-sodium EDTA	ım EDTA
Œ	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC
R51 MRSA	1	10	1	9	<0.5	1	<0.5	<0.5	<0.5	<0.5
R92 MRSA		∞		>15	<0.5	10	<0.5	<0.5	<0.5	<0.5
S93 MRSA		∞		10	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
J67 MRSA		8		10	<0.5	10	<0.5	<0.5	<0.5	<0.5
R8 VRE	<0.5	∞	<0.5	15	<0.5	100	<0.5	20	<0.5	30
Woods VRE		∞		>15	<0.5	100	<0.5	2	<0.5	
S77 Enterococcus Faecium	<0.5	∞	<0.5	15	<0.5	100	<0.5	20	<0.5	9
S76 Enterococcus faecalis		15		15	<0.5	100	<0.5	1.5	<0.5	40
68 Klebsiella pneumoniae	1.5	15	4	>10	∞	09	20	40	9	9
R51 Klebsiella pneumoniae		15	1.5	>10					1 2 2	
128 Klebsiella oxytoca	1	15	-1	>10		06	4	20	4	9
J7 Klebsiella ornitholytica	, 4	>15	1	>10	1	09	20	70	4	8
250 E. coli	1	>15	1	>10	1.5	08	10	20	1.5	1.5
B/C E. coli	1	15	1.5	>10	-					

FIGURE 1C

Organism	Di-potassium EDTA		Di-ammonium EDTA	um EDTA	Di-sodium EDTA	n EDTA	Tri- sodi	Tri- sodium EDTA	Tetra-sodium EDTA	ım EDTA
Œ	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC
137 E. coli	1	15	4	>10	4	09	4	10	2	2
292 Ent. cloacae	4	15	4	>10	4	>100	20	20	9	15
190 Ent. cloacae	4	>15	4	>10	4	100	20	20	9	15
J22 Ent. cloacae	9	>15	<0.5	>10	9	>100	20	20	9	10
R4 Steno. maltophilia	<0.5	10		>10					 	L ()
B/C Pseudomonas aeruginosa		>15	1	>10	1		-			-
J20 Pseudomonas aeruginosa	_	>15		>10	<0.5	50	4	20	2	4
J26 Pseudomonas sp.	1	15	<0.5	>10	<0.5	25	4	9	8	4
R75 Coryne. amycolatum	<0.5	<0.5	<0.5	1	NG	NG	NG	NG	<0.5	20
R23 Coryne. strait/amy	<0.5	<0.5	<0.5	1	NG	9N	9N	NG	<0.5	<0.5
177 Acinetobacter baumanii	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5	<0.5
J44 Acinetobacter baumanii	<0.5	02-09	<0.5	>10	<0.5	1	<0.5	<0.5	<0.5	<0.5

FIGURE 1D

	Di-potassium	ussium	Di-ammonium	nonium						
Organism	EDTA	TA	EDTA	TA	Di-sodium EDTA	n EDTA	Tri- sodi	Tri- sodium EDTA	Tetra-sodium EDTA	ım EDTA
Œ	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC	MIC	MBC
R16 Proteus										
mirabilis	<0.5	>15	<0.5	>10	<0.5	50	<0.5	40	<0.5	15
R81 Proteus										
vulgaris	1	>15	<0.5	>10	<0.5	15	<0.5	40	<0.5	&
R26 Proteus										
mirabilis	<0.5	15	<0.5	>10	<0.5	50	<0.5	09	1	15

FIGURE 2

Organism ID	Tetra-sodium MIC	Tetra-sodium MBC	Di-potassium MIC	Di-potassium MBC	Di-ammonium MIC	Di-ammonium MBC
196 Candida						
albicans	0.5	15	0.5	>100	0.5	>100
J92 Candida						
albicans	0.5	15	0.5	>100	0.5	>100
Myc. Candida						
albicans	0.5	0.5	0.5	>100	0.5	>100
198 Candida						
lucitaniae	0.5	9	0.5	>100	0.5	>100
Myc. Candida						
tropicalis	0.5	10	1	>100	1	100
Myc. Candida						
Guilliermondii	0.5	0.5	0.5	>100	0.5	>100
Myc. Candida						
glabrata	0.5	2	0.5	>100	0.5	90
Myc. Candida						
parapsilosis	0.5	8	0.5	>100	0.5	100
196 Candida						
glabrata	0.5	8	0	100	0.5	>100

FIGURE 3A

			Magnesium Di-sodium	Di-sodium		
	Cupric	ric Total	FDTA	TA	Ferric sodium EDTA	um EDTA
Organism	Di-sodium EDIA	LEDIA		. 1	MIC	MBC
	MIC	MBC	MIC	MBC	2007	>30
	50>	<0.5	9	30	07/	200
S24 Staph. epidermidis	5.0	20%	9	30	>20	>30
31 Staph. epidermidis	<0.05	200	2	>30	>20	>30
301 Staph. xylosus	<0.0>	2.0/	15	>30	>20	>30
300 Staph. capitis	<0.5	<0.3	7	>30	>20	>30
146 Staph. lentus	<0.5	<0.5	0	>30	>20	>30
S24 Staph, capitis	<0.5	<0.5	0 1	>30	>20	>30
R& Stanh, simulans	<0.5	<0.5	C.1	>30	>20	>30
77 Saureus	<0.5	<0.5	>30	>30	>20	>30
R 57 S. aureus	<0.5	<0.5	>30	>30	>20	>30
D13 Saurens	<0.5	<0.5	730	/30	>20	>30
NIO Diamona	<0.5	<0.5	>30	06/		/30
R30 S.aureus	<0.5	<0.5	>30	>30	07<	300
8 S.aureus	200	<0>	>30	>30	>20	>30
R64 MRSA	5.0/	200	>30	>30	>20	>30
R51 MRSA	<0.5	5.0.5	>30	>30	>20	>30
R92 MRSA	<0.5	50.5	>30	>30	>20	>30
S93 MRSA	<0.5	5.0>	>30	>30	>20	>30
J67 MRSA	<0.5	5.0	25	>30	2	>30
R8 VRE	<0.5	C.U.>	730	>30	>20	>30
Woods VRE	>30	>30	7.50	>30	4	>30
e77 Entero-coccus faecium	<0.5	<0.5	C.I	05/	4	>30
SII Lines coons facilie	<0.5	<0.5	>30	05/	118	>15
S/6 Entero-coccus raccarra	>30	>30	>30	>30	CIV.	/15
68 Klebsiella pneumoniae	>30	>30	>30	>30	cl	CIZ
R51 Klebsiella pneumoniae	000					

FIGURE 3B

		_			_		_	Τ	T		_		_												
um EDTA	MBC	747		<u> </u>	>15	>15	>15	115	CIV	>15	>15	>15	>15	115	CI >	>15	10	10	10	>15		2	>15	>15	
Ferric sodium EDTA	DIY	IMITO	CI<	15	15	>15	>15		>I5	>15	>15	10	15		15	15	10	10	9	114	CI	>15	>15	>15	
oi-sodium	1	MBC	>30	>30	>30	>30	000	>30	>30	>30	>30	>30	000	730	>30	>30	4	4	20%	5.0/	>30	>30	30	>30	
Magnesium Di-sodium	1	MIC	>30	>30	230	000	>30	>30	>30	>30	200	05/	>30	>30	08<	>30	200	5.0>	50.5	<0.5	>30	>30	230	000	00%
ric	n EDTA	MBC	>30	200	00/	>30	>30	>30	730	000	>30	×	>30	>30	730	000	>30	<0.5	<0.5	<0.5	15	200	06/	>30	>30
Cupric	Di-sodium EDTA	MIC	027	>30	>30	>30	9	>30	000	>30	>30	9	9	>30	05/	>30	>30	<0.5	<0.5	<0.5	7	0	9	>30	9
	Organism		CII.	128 Klebsiella oxytoca	17 Klebsiella ornitholytica		230 E. COII	B/C E. coll	137 E. coli	292 Firt. cloacae	100 Ent cloacae	100 Ent cloacae	JZZ Lint. Clouduc	R4 Steno. mailtopinna	B/C Pseudomonas aeruginosa	120 Pseudomonas aeruginosa	126 Peeudomonas SD.	D75 Corvme amvcolatum	. 1	K23 Col yile, su and and	177 Acinetobacter Daumann	144 Acinetobacter baumanii	R16 Proteus mirabilis	D&1 Proteits Villearis	TOT Trous mirebilie

FIGURE 4A

	Cul	Cupric				
Organism	Di-sodium+ tetrasodium EDTA	tetrasodium TA	Cupric Di Di-potassi	Cupric Di-sodium + Di-potassium EDTA	Cupric Di-sodium + Di-ammonium EDTA	Cupric Di-sodium + Di-ammonium EDTA
ID	MIC	MBC	MIC	MBC	MIC	MBC
S24 Staph. epidermidis	0.25	2	0.25	15	0.5	20
31 Staph. epidermidis	0.25	8	0.25	20	0.5	20
301 Staph. xylosus	<0.1	>20	<0.1	>20	<0.1	20
300 Staph. capitis	<0.1	>20	<0.1	20	<0.1	20
J46 Staph. lentus	0.25	9	0.25	15	0.5	20
S24 Staph. capitis	0.25	8	0.25	20	0.5	20
R8 Staph. simulans	0.25	>20	l	>20	1	20
72 S.aureus	<0.1	>20	<0.1	>20	<0.1	20
R57 S.aureus	<0.1	>20	<0.1	20	<0.1	20
R13 S.aureus	<0.1	>20	<0.1	20	<0.1	>20
R30 S.aureus	<0.1	15	<0.1	20	<0.1	>20
8 S.aureus	<0.1	>20	<0.1	>20	<0.1	20
R64 MRSA	<0.1	>20	<0.1	>20	<0.1	>20
R51 MRSA	<0.1	>20	<0.1	20	<0.1	>20

FIGURE 4B

	Cui	Cupric				
	Di-sodium + tetrasodium	tetrasodium	Cupric Di	Cupric Di-sodium +	Cupric Di	Cupric Di-sodium +
Organism	ED	EDTA	Di-potassi	Di-potassium EDTA	Di-ammonium EDTA	ium EDTA
ID	MIC	MBC	MIC	MBC	MIC	MBC
R92 MRSA	<0.1	>20	<0.1	>20	<0.1	>20
S93 MRSA	<0.1	15	<0.1	20	<0.1	20
J67 MRSA	<0.1	>20	<0.1	20	<0.1	20
R8 VRE	0.25	20	0.25	20	0.5	>20
Woods VRE	0.25	>20	<0.1	20	<0.1	>20
S77 Entero-coccus faecium	0.5	>20	0.5	>20	1	>20
S76 Entero-coccus faecalis	0.25	>20	<0.1	>20	<0.1	>20
68 Klebsiella pneumoniae	10	>20	9	>20	2	>20
R51 Klebsiella pneumoniae	4	>20	4	>20	2	>20
128 Klebsiella oxytoca	4	>20	2	>20	2	>20
J7 Klebsiella ornitholytica	9	>20	2	>20	2	>20
250 E. coli	9	15	2	>20	2	>20
B/C E. coli	9	1	2	>20	2	>20
137 E. coli	9	4	2	>20	2	>20
292 Ent. cloacae	20	>20	8	>20	8	>20

FIGURE 4C

	Cul	Cupric				
	Di-sodium + tetrasodium	tetrasodium	Cupric Di	Cupric Di-sodium +	Cupric Di	Cupric Di-sodium +
Organism	EDTA	TA	Di-potassi	Di-potassium EDTA	Di-ammon	Di-ammonium EDTA
D	MIC	MBC	MIC	MBC	MIC	MBC
190 Ent. cloacae	20	>20	8	>20	9	>20
J22 Ent. cloacae	20	>20	8	>20	9	>20
R4 Steno. maltophilia	9	10	1	>20	1	>20
B/C Pseudo-monas aeruginosa	9	10	2	>20	2	>20
J20 Pseudo-monas aeruginosa	9	15	2	>20	2	>20
J26 Pseudo-monas sp.	9	>20	2	>20	2	>20
R75 Coryne. amycolatum	<0.1	<0.1	0.25	0.25	0.25	0.25
R23 Coryne. strait/amy	9	10	1	>20	1	>20
177 Acineto-bacter baumanii	9	0.5	0.5	0.25	0.25	<0.1
J44 A. baumanii	9	>20	2	>20	1	>20
R16 Proteus mirabilis	9	>20	2	>20	1	>20
R81 Proteus vulgaris	9	>20	2	>20	2	>20
R26 Proteus mirabilis	9	>20	2	>20	1	>20

FIGURE 5A

																_	1	-		\			T	\neg	
Di- ammonium +	Di-potassium EDTA	MBC	8<		∞ ^		<u></u>		∞		8^		8<		<u></u>		8	8<	0	000	×		& ^	>8<	
Di- amı	Di-potass	MIC	0.5		0.5		0.5		0.5		0.5		0.5		0.5		0.5					1	1	0.5	
Tetracodium +	Di-potassium EDTA	MBC	000	0	9)	>20		>20	2	\ \	o	×)	>20) 	20	000	20		4	20	20	20)
Tetraco	Di-notassi	MIC	IMILY.	-	-		-	1	-	-	90	0.0	3 0	C.O	0.5	C.O	30	6.0	1	0	1				T T
	Tetrasodium +	Ul-ammonium EU1A	MBC	>20		07<		07.<		>20		>20		>20		07<		>20	>20	0	4	>20	067	07/	07<
	Tetraso	D1-ammon	MIC	0.5		0.5		0.5		0.5		0.5		0.5		0.5		1	1	0	-	-			1
		Organism		S24 Staph.	epidermidis	31 Staph.	epidermidis	301 Staph.	xylosus	300 Staph.	capitis	J46 Staph.	lentus	S24 Staph.	capitis	R8 Staph.	simulans	72 Saureus	P57 Saureus	D13 Saurens	DOO Courens	K30 S.aurcus	8 S.aureus	R64 MRSA	R51 MRSA

FIGURE 5B

	Tetras	Tetrasodium +	Tetra	Tetrasodium +	Di- amı	Di- ammonium +
Organism	Di-ammo	Di-ammonium EDTA	Di-pota	Di-potassium EDTA	Di-potass	Di-potassium EDTA
D	MIC	MBC	MIC	MBC	MIC	MBC
R92 MRSA	1	>20	1	>20	1	>8
S93 MRSA	1	>20	1	20	1	8
J67 MRSA	1	>20	1	>20	1	8
R8 VRE	1	>20	1	>20	1	>8
Woods VRE	1	>20	1	>20	1	8<
S77 Entero-coccus faecium	0.5	>20	1	>20	1	>8
S76 Entero-coccus faecalis	1	>20	1	>20	1	>8
68 Klebsiella pneumoniae	>20	>20	>20	>20	10	>10
R51 Klebsiella	1	>20	1	>20	1	>10
pneumoniae						
128 Klebsiella oxytoca	1	>20	1	>20	1	>10
J7 Klebsiella ornitholytica	>20	>20	20	>20	10	>10
250 E. coli	>20	>20	20	>20	2	>10
B/C E. coli	1	0.5	1	1	0.5	>10
137 E. coli	4	>20	20	>20	1	>10
292 Ent. cloacae	8	>20	>20	>20	4	>10

FIGURE 5C

				_	<u> </u>																	,			\bigcap	
Di- ammonium +	Di-potassium EDTA	MBC	>10	>10	710	01<	710		>10		>10		2		0.5		>10		>10	>10		>10		>10		
Di- amı	Di-potass	MIC	y		4	0.5		7	2	1	2	l	0.5	1	0.5		0.5		2	0.5))	0.5	<u>.</u>	2		
diim +	um EDTA	MBC	00	07<	>20	>20		15	00	07	000	07/	-	-	0.5	9	000	07/	>20	07/	07/	220	27	>20		
+ muiposouton	Lettasoutur Di-notassium	MIC	IMIIC	>20	>20			15	4.	51		07	0	0.5	30	C.0 _		٦.		720		•	-	000	07/	
	lium +	um EDIA	MBC	>20	>20	>20		>20		>20		>20		4	4	6.0		∞		>20	>20		>20		07<	
	Tetrasodium +	D1-ammonium ED1A	MIC	>20	>20	1	٠,	8		9		∞		0.5		0.5		4		>20	1		1		>20	
		Organism		100 Ent cloacae		10acac	K4 Steno.	B/C Pseudo-monas	aeruginosa	J20 Pseudo-monas	aeruginosa	J26 Pseudo-monas	sp.	R75 Coryne.	amycolatum	R23 Coryne.	strait/amy	177 Acinetobacter	baumanii	J44 A. baumanii	R16 Proteus	mirabilis	R81 Proteus	vulgaris	R26 Proteus	mirabilis

IGURE 6

	Tetra-sodium FDTA MBEC
	(mg/m) w/v)
Organism	07 VC
31 Staph. epidermidis	70-40
301 Staph. xylosus	20-40
300 Staph, capitis	\$
146 Staph. lentus	. <5
R8 Stanh. simulans	20-40
72 Staph, aureus	<>
R 57 Stanh aureus	\$>
8 Stanh aureus	<5
B92 MRSA	<5
SO3 MRSA	<5
TET MRS A	<>
70 Vlobeielle nneumoniae	<>
17 171-1-1011s omitholytica	<>
J/ Klebsicila Olinciolynca	<5
292 Enteropaciei Cioacac	20
190 Enterobacter cloacae	25
J22 Enterobacter cloacae	CI
R4 Stenotrophomonas maltophilia	<20
120 Pseudomonas aeruginosa	<10
126 Pseudomonas aeruginosa	<5
144 Acinetobacter baumanii	10
R16 Proteus mirabilis	<\$
R81 Proteus vulgaris	<>
H Enterococciis	<5
7097651 E. coli	<5
	<10
7115649 Klebsiella oxytoca	<5
/11001/12000	

IGURE 7

Catheter	EDTA	Colony	Colony	Colony	Colony	Organisms Present
Œ	Conc.	count at	count at	count at	count at	
)	(mg/mL)	0 hours	3 hours	6 hours	24 hours (cfu/mL)	
Ð	40	>100000	120000	0009	0	Mixed Gram-ve and
						Gram+ve cultures
Н	40	>100000	80000	0	0	Mixed Gram-ve and
						Gram+ve cultures
I	40	200000	>500000	25000	0	CNS + Coryneforms
ſ	40	000005<	180000	0	0	CNS
K	40	>1000000	000009	500000	180000	Streptococcus sp.,
						CNS and Gram-ve
						bacillus
Ъ	40	>200000	2500000	150000	54500	Pseudomonas sp. +
						Streptococcus sp.
δ	40	205000	650000	1000	5500	Enterococcus sp.
R	40	2000	500	0	0	MRSA
S	40	>500000	100000	30000	0	CNS
T	40	137500	1000	0	0	MRSA
Ω	40	>200000	182500	00529	13500	CNS
>	40	200000	38500	37500	13000	CNS + Group D
						Streptococcus
W	40	>500000	0	0	0	Enterobacter cloacae
X	40	>200000	20000	0	0	Mixed CNS
2	40	>200000	0	0	0	CNS
A1	40	700000	37000	00009	0	MRSA
B1	40	24000	0	0	0	MRSA

FIGURE 8

Catheter	EDTA	Colony	Colony	Colony	Colony	Organisms Present
1	Conc.	count at	count at	count at	count at	
3	(mg/mL)	0 hours	3 hours	6 hours	24 hours	
		(cfu/mL)	(cfu/mL)	(cfu/mL)	(cfu/mL)	
A	100	100000000	0	0	0	CNS
В	100	10000000	100	200	0	CNS
C	50	100000000	0	0	0	Mixed coliforms
D	20	>100000	250000	100000	0	Mixed Gram-ve and
						Gram+ve cultures
H	30	>100000	400000	360000	0	Mixed Gram-ve and
						Gram+ve cultures
Ŧ	30	300000	00025	2000	0	Mixed Gram-ve and
						Gram+ve cultures
Γ	09	000009	0005	4000	0	Enterococcus sp.
M	09	>500000	300000	17000	17000	Proteus sp. and CNS
0	50	200000	30000	130000	0	Staphylococcus aureus
Z	50	200000	10000	0	0	CNS
(arterial)						
Z	90	300000	10000	00009	0	Klebsiella pneumoniae
(snoues)			(CNS	(CNS		+ CNS
			only)	only)		